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RAW SEQUENCE LISTING
PATENT APPLICATION US/08/014,096

DATE: 09/28/93
TIME: 10:23:43

INPUT SET: S586.raw

SEQUENCE LISTING

ENTERED

1
2
3 (1) General Information:
4
5 (i) APPLICANT: Huston, James S
6 Charette, Marc F
7 Cohen, Charles M
8 Crea, Roberto
9 Keck, Peter C
10 Oppermann, Hermann
11 Rueger, David C
12 Ridge, Richard J
13
14 (ii) TITLE OF INVENTION: Product and Process for the Production,
15 Isolation and Purification of Recombinant Polypeptides
16
17 (iii) NUMBER OF SEQUENCES: 14
18
19 (iv) CORRESPONDENCE ADDRESS:
20 (A) ADDRESSEE: Creative BioMolecules
21 (B) STREET: 35 South Street
22 (C) CITY: Hopkinton
23 (D) STATE: MA
24 (E) COUNTRY: USA
25 (F) ZIP: 01748
26
27 (v) COMPUTER READABLE FORM:
28 (A) MEDIUM TYPE: Floppy disk
29 (B) COMPUTER: IBM PC compatible
30 (C) OPERATING SYSTEM: PC-DOS/MS-DOS
31 (D) SOFTWARE: PatentIn Release #1.0, Version #1.25
32
33 (vi) CURRENT APPLICATION DATA:
34 (A) APPLICATION NUMBER: US/08/014,096
35 (B) FILING DATE:
36 (C) CLASSIFICATION:
37
38 (vii) PRIOR APPLICATION DATA:
39 (A) APPLICATION NUMBER: US 07/661,070
40 (B) FILING DATE: 26-FEB-1991
41
42 (viii) ATTORNEY/AGENT INFORMATION:
43 (A) NAME: Lunn, Paul G.
44 (B) REGISTRATION NUMBER: 32,743
45 (C) REFERENCE/DOCKET NUMBER: CRP-008DV
46
47 (ix) TELECOMMUNICATION INFORMATION:
48 (A) TELEPHONE: (508) 435-9001
49 (B) TELEFAX: (508) 435-6951
50
51

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52 (2) INFORMATION FOR SEQ ID NO:1:
53
54 (i) SEQUENCE CHARACTERISTICS:
55 (A) LENGTH: 4 amino acids
56 (B) TYPE: amino acid
57 (C) STRANDEDNESS: single
58 (D) TOPOLOGY: linear
59
60 (ii) MOLECULE TYPE: peptide
61
62 (iii) HYPOTHETICAL: NO
63
64 (iv) ANTI-SENSE: NO
65
66 (v) FRAGMENT TYPE: internal
67
68
69
70 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:
71
72 Ile Glu Gly Arg
73 1
74
75 (2) INFORMATION FOR SEQ ID NO:2:
76
77 (i) SEQUENCE CHARACTERISTICS:
78 (A) LENGTH: 21 base pairs
79 (B) TYPE: nucleic acid
80 (C) STRANDEDNESS: double
81 (D) TOPOLOGY: linear
82
83 (ii) MOLECULE TYPE: cDNA
84
85 (iii) HYPOTHETICAL: NO
86
87 (iv) ANTI-SENSE: NO
88
89 (v) FRAGMENT TYPE: N-terminal
90
91
92 (ix) FEATURE:
93 (A) NAME/KEY: CDS
94 (B) LOCATION: 1..21
95
96
97 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:
98
99 GCT AAA AAC CTT AAC GAA GCT
100 Ala Lys Asn Leu Asn Glu Ala
101 1 5
102

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103
104 (2) INFORMATION FOR SEQ ID NO:3:
105
106 (i) SEQUENCE CHARACTERISTICS:
107 (A) LENGTH: 7 amino acids
108 (B) TYPE: amino acid
109 (D) TOPOLOGY: linear
110
111 (ii) MOLECULE TYPE: protein
112
113 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:3:
114
115 Ala Lys Asn Leu Asn Glu Ala
116 1 5
117
118 (2) INFORMATION FOR SEQ ID NO:4:
119
120 (i) SEQUENCE CHARACTERISTICS:
121 (A) LENGTH: 13 amino acids
122 (B) TYPE: amino acid
123 (C) STRANDEDNESS: single
124 (D) TOPOLOGY: linear
125
126 (ii) MOLECULE TYPE: peptide
127
128 (iii) HYPOTHETICAL: NO
129
130 (iv) ANTI-SENSE: NO
131
132 (v) FRAGMENT TYPE: internal
133
134
135
136 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:4:
137
138 Met Lys Ala Ile Phe Val Leu Lys Gly Ser Leu Asp Glu
139 1 5 10
140
141 (2) INFORMATION FOR SEQ ID NO:5:
142
143 (i) SEQUENCE CHARACTERISTICS:
144 (A) LENGTH: 16 amino acids
145 (B) TYPE: amino acid
146 (C) STRANDEDNESS: single
147 (D) TOPOLOGY: linear
148
149 (ii) MOLECULE TYPE: peptide
150
151 (iii) HYPOTHETICAL: NO
152
153 (iv) ANTI-SENSE: NO

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154
155 (v) FRAGMENT TYPE: internal
156
157
158
159 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:5:
160
161 Met Lys Ala Ile Phe Val Leu Lys Gly Ser Leu Asp Arg Asp Leu Glu
162 1 5 10 15
163
164
165 (2) INFORMATION FOR SEQ ID NO:6:
166
167 (i) SEQUENCE CHARACTERISTICS:
168 (A) LENGTH: 59 amino acids
169 (B) TYPE: amino acid
170 (C) STRANDEDNESS: single
171 (D) TOPOLOGY: linear
172
173 (ii) MOLECULE TYPE: protein
174
175 (iii) HYPOTHETICAL: NO
176
177 (iv) ANTI-SENSE: NO
178
179 (v) FRAGMENT TYPE: N-terminal
180
181
182
183 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:6:
184
185 Met Lys Ala Ile Phe Val Leu Lys Gly Ser Leu Asp Arg Asp Leu Asp
186 1 5 10 15
187
188 Ser Arg Leu Asp Leu Asp Val Arg Thr Asp His Lys Asp Leu Ser Asp
189 20 25 30
190
191 His Leu Val Leu Val Asp Leu Ala Arg Asn Asp Leu Ala Arg Ile Val
192 35 40 45
193
194 Thr Pro Gly Ser Arg Tyr Val Ala Asp Leu Glu
195 50 55
196
197 (2) INFORMATION FOR SEQ ID NO:7:
198
199 (i) SEQUENCE CHARACTERISTICS:
200 (A) LENGTH: 4 amino acids
201 (B) TYPE: amino acid
202 (C) STRANDEDNESS: single
203 (D) TOPOLOGY: linear
204

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205 (ii) MOLECULE TYPE: peptide
206
207 (iii) HYPOTHETICAL: NO
208
209 (iv) ANTI-SENSE: NO
210
211 (v) FRAGMENT TYPE: internal
212
213
214
215 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:7:
216
217 Glu Phe Met Arg
218 1
219
220 (2) INFORMATION FOR SEQ ID NO:8:
221
222 (i) SEQUENCE CHARACTERISTICS:
223 (A) LENGTH: 10 amino acids
224 (B) TYPE: amino acid
225 (C) STRANDEDNESS: single
226 (D) TOPOLOGY: linear
227
228 (ii) MOLECULE TYPE: peptide
229
230 (iii) HYPOTHETICAL: NO
231
232 (iv) ANTI-SENSE: NO
233
234 (v) FRAGMENT TYPE: internal
235
236
237
238 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:8:
239
240 Glu Phe Asp Pro Pro Pro Lys Phe Met Arg
241 1 5 10
242
243 (2) INFORMATION FOR SEQ ID NO:9:
244
245 (i) SEQUENCE CHARACTERISTICS:
246 (A) LENGTH: 13 amino acids
247 (B) TYPE: amino acid
248 (C) STRANDEDNESS: single
249 (D) TOPOLOGY: linear
250
251 (ii) MOLECULE TYPE: peptide
252
253 (iii) HYPOTHETICAL: NO
254
255 (iv) ANTI-SENSE: NO

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256
257 (v) FRAGMENT TYPE: internal
258
259
260
261 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:9:
262
263 Glu Phe Asp Pro Pro Met Pro Arg Lys Phe Met Arg
264 1 5 10
265
266 (2) INFORMATION FOR SEQ ID NO:10:
267
268 (i) SEQUENCE CHARACTERISTICS:
269 (A) LENGTH: 20 amino acids
270 (B) TYPE: amino acid
271 (C) STRANDEDNESS: single
272 (D) TOPOLOGY: linear
273
274 (ii) MOLECULE TYPE: peptide
275
276 (iii) HYPOTHETICAL: NO
277
278 (iv) ANTI-SENSE: NO
279
280 (v) FRAGMENT TYPE: internal
281
282
283
284 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:10:
285
286 Glu Phe Asp Pro Pro Pro Met Pro Arg Met Pro Asp Pro Glu Leu Arg
287 1 5 10 15
288
289 Lys Phe Met Arg
290 20
291
292 (2) INFORMATION FOR SEQ ID NO:11:
293
294 (i) SEQUENCE CHARACTERISTICS:
295 (A) LENGTH: 193 amino acids
296 (B) TYPE: amino acid
297 (C) STRANDEDNESS: single
298 (D) TOPOLOGY: linear
299
300 (ii) MOLECULE TYPE: protein
301
302 (iii) HYPOTHETICAL: NO
303
304 (iv) ANTI-SENSE: NO
305
306 (v) FRAGMENT TYPE: N-terminal

RAW SEQUENCE LISTING
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307
308
309
310 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:11:
311
312 Met Lys Ala Ile Phe Val Leu Lys Gly Ser Leu Asp Arg Asp Leu Asp
313 1 5 10 15
314
315 Ser Arg Ile Glu Leu Glu Met Arg Thr Asp His Lys Glu Leu Ser Glu
316 20 25 30
317
318 His Leu Met Leu Val Asp Leu Ala Arg Asn Asp Leu Ala Arg Ile Cys
319 35 40 45
320
321 Thr Pro Gly Ser Arg Tyr Val Ala Asp Leu Thr Lys Val Asp Arg Tyr
322 50 55 60
323
324 Ser Tyr Val Met His Leu Val Ser Arg Val Val Gly Glu Leu Arg His
325 65 70 75 80
326
327 Asp Leu Asp Ala Leu His Ala Tyr Arg Ala Cys Met Asn Met Gly Thr
328 85 90 95
329
330 Leu Ser Gly Ala Pro Lys Val Arg Ala Met Gln Leu Ile Ala Glu Ala
331 100 105 110
332
333 Glu Gly Arg Arg Arg Gly Ser Tyr Gly Gly Ala Val Gly Tyr Phe Thr
334 115 120 125
335
336 Ala His Gly Asp Leu Asp Thr Cys Ile Val Ile Arg Ser Ala Leu Val
337 130 135 140
338
339 Glu Asn Gly Ile Ala Thr Val Gln Ala Gly Ala Gly Val Val Leu Asp
340 145 150 155 160
341
342 Ser Val Pro Gln Ser Glu Ala Asp Glu Thr Arg Asn Lys Ala Arg Ala
343 165 170 175
344
345 Val Leu Arg Ala Ile Ala Thr Ala His His Ala Gln Glu Phe Pro Gly
346 180 185 190
347
348 Glu
349
350

351 (2) INFORMATION FOR SEQ ID NO:12:
352

353 (i) SEQUENCE CHARACTERISTICS:
354 (A) LENGTH: 59 amino acids
355 (B) TYPE: amino acid
356 (C) STRANDEDNESS: single
357 (D) TOPOLOGY: linear

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358
359 (ii) MOLECULE TYPE: protein
360
361 (iii) HYPOTHETICAL: NO
362
363 (iv) ANTI-SENSE: NO
364
365 (v) FRAGMENT TYPE: N-terminal
366
367
368
369 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:12:
370
371 Met Lys Ala Ile Phe Val Leu Lys Gly Ser Leu Asp Arg Asp Leu Asp
372 1 5 10 15
373
374 Ser Arg Leu Asp Leu Asp Val Arg Thr Asp His Lys Asp Leu Ser Asp
375 20 25 30
376
377 His Leu Val Leu Val Asp Leu Ala Arg Asn Asp Leu Ala Arg Ile Val
378 35 40 45
379
380 Thr Pro Gly Ser Arg Tyr Val Ala Asp Leu Glu
381 50 55
382
383 (2) INFORMATION FOR SEQ ID NO:13:
384
385 (i) SEQUENCE CHARACTERISTICS:
386 (A) LENGTH: 21 amino acids
387 (B) TYPE: amino acid
388 (C) STRANDEDNESS: single
389 (D) TOPOLOGY: linear
390
391 (ii) MOLECULE TYPE: peptide
392
393 (iii) HYPOTHETICAL: NO
394
395 (iv) ANTI-SENSE: NO
396
397 (v) FRAGMENT TYPE: internal
398
399
400
401 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:13:
402
403 Met Lys Ala Ile Phe Val Leu Lys Gly Ser Leu Asp Arg Asp Leu Glu
404 1 5 10 15
405
406 Phe Met Pro Pro Cys
407 20
408

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409 (2) INFORMATION FOR SEQ ID NO:14:

410

411 (i) SEQUENCE CHARACTERISTICS:

412 (A) LENGTH: 19 amino acids

413 (B) TYPE: amino acid

414 (C) STRANDEDNESS: single

415 (D) TOPOLOGY: linear

416

417 (ii) MOLECULE TYPE: peptide

418

419 (iii) HYPOTHETICAL: NO

420

421 (iv) ANTI-SENSE: NO

422

423 (v) FRAGMENT TYPE: internal

424

425

426

427 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:14:

428

429 Met Lys Ala Ile Phe Val Leu Lys Gly Ser Leu Asp Arg Asp Leu Glu

430 1 5 10 15

431

432 Phe Met Cys

433

434

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SEQUENCE VERIFICATION REPORT
PATENT APPLICATION US/08/014,096

DATE: 09/28/93
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| Line | Error | Original Text |
|------|---------------------------------|---------------------------------------|
| 34 | Wrong application Serial Number | (A) APPLICATION NUMBER: US/08/014,096 |

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SEQUENCE MISSING ITEM REPORT
PATENT APPLICATION *US/08/014,096*

DATE: 09/28/93
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INPUT SET: S586.raw

< < THERE ARE NO ITEMS MISSING > >

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SEQUENCE CORRECTION REPORT
PATENT APPLICATION US/08/014,096

DATE: 09/28/93
TIME: 10:24:51

INPUT SET: S586.raw

Line

Original Text

Corrected Text